

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/538,767
Source: PCT
Date Processed by STIC: 06/21/2005

ENTERED



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/538,767

DATE: 06/21/2005

TIME: 13:49:24

Input Set : A:\SequenceListing.ST25.txt
 Output Set: N:\CRF4\06172005\J538767.raw

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4 <110> APPLICANT: Ottawa Health Research Institute
5 Megeney, Lynn
7 <120> TITLE OF INVENTION: MODULATION OF STEM CELL DIFFERENTIATION
8 BY MODULATION OF CASPASE-3 ACTIVITY
11 <130> FILE REFERENCE: 241-137PCT
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/538,767
C--> 14 <141> CURRENT FILING DATE: 2005-06-10
16 <150> PRIOR APPLICATION NUMBER: US 60/431,991
17 <151> PRIOR FILING DATE: 2002-12-10
19 <150> PRIOR APPLICATION NUMBER: US 60/431,990
20 <151> PRIOR FILING DATE: 2002-12-10
22 <160> NUMBER OF SEQ ID NOS: 10
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 835
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
W--> 32 <221> NAME/KEY:
33 <222> LOCATION:
34 <223> OTHER INFORMATION: human caspase-3 gene
36 <400> SEQUENCE: 1
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38 catacatgga agcgaatcaa tggactctgg aatatccctg gacaacagtt ataaaaatgga 120
39 ttatcctgag atgggtttat gtataataat taataataag aattttcata aaagcactgg 180
40 aatgacatct cggctctggta cagatgtcga tgcagcaaac ctcaggaaa cattcagaaa 240
41 cttgaaatat gaagtcaagga ataaaaatga tcttacacgt gaagaaaattt tggaatttgat 300
42 gcgtgatgtt tctaaagaag atcacagcaa aaggagcagt tttgtttgtg tgcttctgag 360
43 ccatggtgaa gaaggaataa ttttggAAC aaatggacct gttgacactga aaaaaataaac 420
44 aaacttttc agaggggatc gttgttagaag tctaactgga aaacccaaac ttttcattat 480
45 tcaggcctgc cgtggtagac aactggactg tggcatttag acagacagtg gtgttgatga 540
46 tgacatggcg tgcataaaa taccagtgg a gccgacttc ttgttatgcat actccacagc 600
47 acctggatat tattcttggc gaaattcaaa ggatggctcc tggttcatcc agtcgctttg 660
48 tgccatgctg aaacagatag ccgacaagct tgaattttag cacattctt cccgggttaa 720
49 cggaaagggtg gcaacagaat ttgagtcctt ttccttgac gctacttttc atgcaaagaa 780
50 acagattcca tgtattgttt ccatgctcac aaaagaactc tatttttatac actaa 835
52 <210> SEQ ID NO: 2
53 <211> LENGTH: 277
54 <212> TYPE: PRT
55 <213> ORGANISM: Homo sapiens
57 <400> SEQUENCE: 2
58 Met Glu Asn Thr Glu Asn Ser Val Asp Ser Lys Ser Ile Lys Asn Leu
59 1 5 10 15

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60 Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser
 61 20 25 30
 62 Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile
 63 35 40 45
 64 Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg
 65 50 55 60
 66 Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn
 67 65 70 75 80
 68 Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile
 69 85 90 95
 70 Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser
 71 100 105 110
 72 Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Gly Ile Ile Phe
 73 115 120 125
 74 Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg
 75 130 135 140
 76 Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
 77 145 150 155 160
 78 Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
 79 165 170 175
 80 Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp
 81 180 185 190
 82 Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn
 83 195 200 205
 84 Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys
 85 210 215 220
 86 Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn
 87 225 230 235 240
 88 Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe
 89 245 250 255
 90 His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu
 91 260 265 270
 92 Leu Tyr Phe Tyr His
 93 275
 96 <210> SEQ ID NO: 3
 97 <211> LENGTH: 1910
 98 <212> TYPE: DNA
 99 <213> ORGANISM: Homo sapiens
 101 <220> FEATURE:
 W--> 102 <221> NAME/KEY:
 103 <222> LOCATION:
 104 <223> OTHER INFORMATION: human MST1 gene
 106 <400> SEQUENCE: 3
 107 ccggctgctg gcatcgccca tggagacggt acagctgagg aaccgcgcgc gccggcagct 60
 108 gaaaaagttt gatgaagata gtttaaccaa acaaccagaa gaagtatttg atgtcttaga 120
 109 gaaacttgga gaagggtcct atggcagcgt atacaaaagct attcataaaag agaccggcca 180
 110 gatttgttgcg attaagcaag ttccctgttggaa atcagacctc caggagataa tcaaaagaat 240
 111 ctctataatcg cagcaatgtg acagccctca tgttgtcaaa tattatggca gttatTTAA 300
 112 gaacacagac ttatggatcg ttatggagta ctgtggggct ggttctgtat ctgatatcat 360

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113 tcgattacga aataaaaacgt taacagaaga taaaaatagct acaatattac aatcaactct 420
114 taagggactt gaatacccttc attttatgag aaaaatacac cgagatatca aggcaggaaa 480
115 tattttgcta aatacagaag gacatgcaaa acttgcagat tttggggtag caggtcaact 540
116 tacagatacc atggccaagc ggaatacagt gataggaaca ccattttgga tggctccaga 600
117 agtgattcag gaaattggat acaactgtgt agcagacatc tggtccctgg gaataactgc 660
118 catagaaaatg gctgaaggaa agcgccctta tgctgatatc catccaatga gggcaatctt 720
119 catgattcct acaaattcctc ctccccacatt ccgaaaaacca gagctatggt cagataactt 780
120 tacagattt gtgaaacagt gtcttgtaaa gagccctgag cagagggcca cagccactca 840
121 gctcctgcag cacccatttgc ttaggagtgc caaaggagtgc tcaatactgc gagacttaat 900
122 taatgaagcc atggatgtga aactgaaacg ccaggaatcc cagcagcggg aaatggacca 960
123 ggacgatgaa gaaaactcg aagaggatga aatggattct ggcacgatgg ttgcagcagt 1020
124 ggtgtatgag atgggcactg tccgagtagc cagcaccatg actgtatggag ccaatactat 1080
125 gattgagcac gatgacacgt tgccatcaca actgggcacc atggtgatca atgcagagga 1140
126 ttaggaagag gaaggaacta tggaaaagaag ggtgagacc atgcagcctg cggaaaccatc 1200
127 ctttcttgcgaa tattttgaaac aaaaagaaaaa ggaaaaaccag atcaacagct ttggcaagag 1260
128 tgtacctggt ccactgaaaaa attcttcaga ttggaaaata ccacaggatg gagactacga 1320
129 gtttcttaag agttggacag tggaggacct tcagaagagg ctcttggccc ttggacccat 1380
130 gatggagcag gagattgaaag agatccggca gaagtaccag tccaaggccc agcccatcct 1440
131 ggtatgccata gaggctaaag aagagacggca acaaaaacttc tgagcaaggc caggctgtga 1500
132 gggcccccagc tccaccagg ctttgggtga attctggatg gcttgctcat gtttggtagc 1560
133 cagcaccccttc tgctctgtcg tctctccaca gcacccctgt gaactcagga atgtgcgcc 1620
134 gtttggaaaggc ctctcttgcg agtcagcgtg ccattttgat gtgtgtatgt acattggtca 1680
135 ggttatattat ctcaaaaggat ttatattggg cgactttaa ctcagagttt taaacccca 1740
136 gaacagagac tccctagttga gtgatagctg ggaaagttt acattgtctg tttttcttct 1800
137 cccaatagct ttcaatttgcg ctttcttggaa gactttaaa aaaatataaa tatgcatata 1860
138 tatataaaaa ttataaaatag attccccacg caggttggtg gcattctctgt 1910
140 <210> SEQ ID NO: 4
141 <211> LENGTH: 487
142 <212> TYPE: PRT
143 <213> ORGANISM: Homo sapiens
145 <400> SEQUENCE: 4
146 Met Glu Thr Val Gln Leu Arg Asn Pro Pro Arg Arg Gln Leu Lys Lys
147 1 5 10 15
148 Leu Asp Glu Asp Ser Leu Thr Lys Gln Pro Glu Glu Val Phe Asp Val
149 20 25 30
150 Leu Glu Lys Leu Gly Glu Gly Ser Tyr Gly Ser Val Tyr Lys Ala Ile
151 35 40 45
152 His Lys Glu Thr Gly Gln Ile Val Ala Ile Lys Gln Val Pro Val Glu
153 50 55 60
154 Ser Asp Leu Gln Glu Ile Ile Lys Glu Ile Ser Ile Met Gln Gln Cys
155 65 70 75 80
156 Asp Ser Pro His Val Val Lys Tyr Tyr Gly Ser Tyr Phe Lys Asn Thr
157 85 90 95
158 Asp Leu Trp Ile Val Met Glu Tyr Cys Gly Ala Gly Ser Val Ser Asp
159 100 105 110
160 Ile Ile Arg Leu Arg Asn Lys Thr Leu Thr Glu Asp Glu Ile Ala Thr
161 115 120 125
162 Ile Leu Gln Ser Thr Leu Lys Gly Leu Glu Tyr Leu His Phe Met Arg
163 130 135 140

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164 Lys Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Asn Thr Glu
165 145           150           155           160
166 Gly His Ala Lys Leu Ala Asp Phe Gly Val Ala Gly Gln Leu Thr Asp
167           165           170           175
168 Thr Met Ala Lys Arg Asn Thr Val Ile Gly Thr Pro Phe Trp Met Ala
169           180           185           190
170 Pro Glu Val Ile Gln Glu Ile Gly Tyr Asn Cys Val Ala Asp Ile Trp
171           195           200           205
172 Ser Leu Gly Ile Thr Ala Ile Glu Met Ala Glu Gly Lys Arg Pro Tyr
173           210           215           220
174 Ala Asp Ile His Pro Met Arg Ala Ile Phe Met Ile Pro Thr Asn Pro
175 225           230           235           240
176 Pro Pro Thr Phe Arg Lys Pro Glu Leu Trp Ser Asp Asn Phe Thr Asp
177           245           250           255
178 Phe Val Lys Gln Cys Leu Val Lys Ser Pro Glu Gln Arg Ala Thr Ala
179           260           265           270
180 Thr Gln Leu Leu Gln His Pro Phe Val Arg Ser Ala Lys Gly Val Ser
181           275           280           285
182 Ile Leu Arg Asp Leu Ile Asn Glu Ala Met Asp Val Lys Leu Lys Arg
183           290           295           300
184 Gln Glu Ser Gln Gln Arg Glu Met Asp Gln Asp Asp Glu Glu Asn Ser
185 305           310           315           320
186 Glu Glu Asp Glu Met Asp Ser Gly Thr Met Val Arg Ala Val Gly Asp
187           325           330           335
188 Glu Met Gly Thr Val Arg Val Ala Ser Thr Met Thr Asp Gly Ala Asn
189           340           345           350
190 Thr Met Ile Glu His Asp Asp Thr Leu Pro Ser Gln Leu Gly Thr Met
191           355           360           365
192 Val Ile Asn Ala Glu Asp Glu Glu Glu Gly Thr Met Lys Arg Arg
193           370           375           380
194 Asp Glu Thr Met Gln Pro Ala Lys Pro Ser Phe Leu Glu Tyr Phe Glu
195 385           390           395           400
196 Gln Lys Glu Lys Glu Asn Gln Ile Asn Ser Phe Gly Lys Ser Val Pro
197           405           410           415
198 Gly Pro Leu Lys Asn Ser Ser Asp Trp Lys Ile Pro Gln Asp Gly Asp
199           420           425           430
200 Tyr Glu Phe Leu Lys Ser Trp Thr Val Glu Asp Leu Gln Lys Arg Leu
201           435           440           445
202 Leu Ala Leu Asp Pro Met Met Glu Gln Glu Ile Glu Glu Ile Arg Gln
203           450           455           460
204 Lys Tyr Gln Ser Lys Arg Gln Pro Ile Leu Asp Ala Ile Glu Ala Lys
205 465           470           475           480
206 Lys Arg Arg Gln Gln Asn Phe
207           485
210 <210> SEQ ID NO: 5
211 <211> LENGTH: 30
212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:

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216 <223> OTHER INFORMATION: primer
 218 <400> SEQUENCE: 5
 219 atgaccatga ttacgaattc atggagacac 30
 221 <210> SEQ ID NO: 6
 222 <211> LENGTH: 30
 223 <212> TYPE: DNA
 224 <213> ORGANISM: Artificial Sequence
 226 <220> FEATURE:
 227 <223> OTHER INFORMATION: primer
 229 <400> SEQUENCE: 6
 230 cactcttagat taattaaaaa aatagagttc 30
 232 <210> SEQ ID NO: 7
 233 <211> LENGTH: 268
 234 <212> TYPE: PRT
 235 <213> ORGANISM: Homo sapiens
 237 <400> SEQUENCE: 7
 238 Ser Lys Ser Ile Lys Asn Leu Glu Pro Lys Ile Ile His Gly Ser Glu
 239 1 5 10 15
 240 Ser Met Asp Ser Gly Ile Ser Leu Asp Asn Ser Tyr Lys Met Asp Tyr
 241 20 25 30
 242 Pro Glu Met Gly Leu Cys Ile Ile Asn Asn Lys Asn Phe His Lys
 243 35 40 45
 244 Ser Thr Gly Met Thr Ser Arg Ser Gly Thr Asp Val Asp Ala Ala Asn
 245 50 55 60
 246 Leu Arg Glu Thr Phe Arg Asn Leu Lys Tyr Glu Val Arg Asn Lys Asn
 247 65 70 75 80
 248 Asp Leu Thr Arg Glu Glu Ile Val Glu Leu Met Arg Asp Val Ser Lys
 249 85 90 95
 250 Glu Asp His Ser Lys Arg Ser Ser Phe Val Cys Val Leu Leu Ser His
 251 100 105 110
 252 Gly Glu Glu Gly Ile Ile Phe Gly Thr Asn Gly Pro Val Asp Leu Lys
 253 115 120 125
 254 Lys Ile Thr Asn Phe Phe Arg Gly Asp Arg Cys Arg Ser Leu Thr Gly
 255 130 135 140
 256 Lys Pro Lys Leu Phe Ile Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp
 257 145 150 155 160
 258 Cys Gly Ile Glu Thr Asp Ser Gly Val Asp Asp Asp Met Ala Cys His
 259 165 170 175
 260 Lys Ile Pro Val Glu Ala Asp Phe Leu Tyr Ala Tyr Ser Thr Ala Pro
 261 180 185 190
 262 Gly Tyr Tyr Ser Trp Arg Asn Ser Lys Asp Gly Ser Trp Phe Ile Gln
 263 195 200 205
 264 Ser Leu Cys Ala Met Leu Lys Gln Tyr Ala Asp Lys Leu Glu Phe Met
 265 210 215 220
 266 His Ile Leu Thr Arg Val Asn Arg Lys Val Ala Thr Glu Phe Glu Ser
 267 225 230 235 240
 268 Phe Ser Phe Asp Ala Thr Phe His Ala Lys Lys Gln Ile Pro Cys Ile
 269 245 250 255
 270 Val Ser Met Leu Thr Lys Glu Leu Tyr Phe Tyr His

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:32 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1

L:102 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3